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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/043,774B

DATE: 06/17/2002

TIME: 14:44:59

Input Set: A:\02-0013.st25.txt

Output Set: N:\CRF3\06172002\J043774B.raw

3 <110> APPLICANT: University of Illinois at Chicago
4 Sharma, Arun
5 Hoffman, Ronald
7 <120> TITLE OF INVENTION: HUMAN HEMATOPOIETIC GROWTH REGULATORY GENE AND USES
9 <130> FILE REFERENCE: MBHB: CU08/PPA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/043,774B
C--> 11 <141> CURRENT FILING DATE: 2002-06-06
11 <160> NUMBER OF SEQ ID NOS: 17
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 2328
17 <212> TYPE: DNA
18 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(2328)
23 <223> OTHER INFORMATION: Human Hiwi Protein
26 <400> SEQUENCE: 1
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28 Met Ile Phe Gly Val Asn Thr Arg Gln Asn Leu Asp His Val Lys Glu
29 1 5 10 15
31 tca aaa aca ggt tct tca ggc att ata gta agg tta agc act aac cat 96
32 Ser Lys Thr Gly Ser Ser Gly Ile Ile Val Arg Leu Ser Thr Asn His
33 20 25 30
35 ttc cgg ctg aca tcc cgt ccc cag tgg gcc tta tat cag tat cac att 144
36 Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile
37 35 40 45
39 gac tat aac cca ctg atg gaa gcc aga aga ctc cgt tca gct ctt ctt 192
40 Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu
41 50 55 60
43 ttt caa cac gaa gat cta att gga aag tgt cat gct ttt gat gga acg 240
44 Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr
45 65 70 75 80
47 ata tta ttt tta cct aaa aga cta cag caa aag gtt act gaa gtt ttt 288
48 Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe
49 85 90 95
51 agt aag acc cgg aat gga gag gat gtg agg ata acg atc act tta aca 336
52 Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr
53 100 105 110
55 aat gaa ctt cca cct aca tca cca act tgt ttg cag ttc tat aat att 384
56 Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile
57 115 120 125
59 att ttc agg agg ctt ttg aaa atc atg aat ttg caa caa att gga cga 432

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61		130					135					140					
63	aat	tat	tat	aac	cca	aat	gac	cca	att	gat	att	cca	agt	cac	agg	ttg	480
64	Asn	Tyr	Tyr	Asn	Pro	Asn	Asp	Pro	Ile	Asp	Ile	Pro	Ser	His	Arg	Leu	
65	145					150				155					160		
67	gtg	att	tgg	cct	ggc	ttc	act	act	tcc	atc	ctt	cag	tat	gaa	aac	agc	528
68	Val	Ile	Trp	Pro	Gly	Phe	Thr	Thr	Ser	Ile	Leu	Gln	Tyr	Glu	Asn	Ser	
69					165					170					175		
71	atc	atg	ctc	tgc	act	gac	gtt	agc	cat	aaa	gtc	ctt	cga	agt	gag	act	576
72	Ile	Met	Leu	Cys	Thr	Asp	Val	Ser	His	Lys	Val	Leu	Arg	Ser	Glu	Thr	
73				180					185					190			
75	gtt	ttg	gat	ttc	atg	ttc	aac	ttt	tat	cat	cag	aca	gaa	gaa	cat	aaa	624
76	Val	Leu	Asp	Phe	Met	Phe	Asn	Phe	Tyr	His	Gln	Thr	Glu	Glu	His	Lys	
77			195					200					205				
79	ttt	caa	gaa	caa	gtt	tcc	aaa	gaa	cta	ata	ggg	tta	gtt	gtt	ctt	acc	672
80	Phe	Gln	Glu	Gln	Val	Ser	Lys	Glu	Leu	Ile	Gly	Leu	Val	Val	Leu	Thr	
81		210					215				220						
83	aag	tat	aac	aat	aag	aca	tac	aga	gtg	gat	gat	att	gac	tgg	gac	cag	720
84	Lys	Tyr	Asn	Asn	Lys	Thr	Tyr	Arg	Val	Asp	Asp	Ile	Asp	Trp	Asp	Gln	
85	225					230					235				240		
87	aat	ccc	aag	agc	acc	ttt	aag	aaa	gcc	gac	ggc	tct	gaa	gtc	agc	ttc	768
88	Asn	Pro	Lys	Ser	Thr	Phe	Lys	Lys	Ala	Asp	Gly	Ser	Glu	Val	Ser	Phe	
89				245					250					255			
91	tta	gaa	tac	tac	agg	aag	caa	tac	aac	caa	gag	atc	acc	gac	ttg	aag	816
92	Leu	Glu	Tyr	Tyr	Arg	Lys	Gln	Tyr	Asn	Gln	Glu	Ile	Thr	Asp	Leu	Lys	
93			260					265					270				
95	cag	cct	gtc	ttg	gtc	agc	cag	ccc	aag	aga	agg	cgg	ggc	cct	ggg	ggg	864
96	Gln	Pro	Val	Leu	Val	Ser	Gln	Pro	Lys	Arg	Arg	Arg	Gly	Pro	Gly	Gly	
97			275				280					285					
99	aca	ctg	cca	ggg	cct	gcc	atg	ctc	att	cct	gag	ctc	tgc	tat	ctt	aca	912
100	Thr	Leu	Pro	Gly	Pro	Ala	Met	Leu	Ile	Pro	Glu	Leu	Cys	Tyr	Leu	Thr	
101		290					295				300						
103	ggg	cta	act	gat	aaa	atg	cgt	aat	gat	ttt	aac	gtg	atg	aaa	gac	tta	960
104	Gly	Leu	Thr	Asp	Lys	Met	Arg	Asn	Asp	Phe	Asn	Val	Met	Lys	Asp	Leu	
105	305					310					315				320		
107	gcc	gtt	cat	aca	aga	cta	act	cca	gag	caa	agg	cag	cgt	gaa	gtg	gga	1008
108	Ala	Val	His	Thr	Arg	Leu	Thr	Pro	Glu	Gln	Arg	Gln	Arg	Glu	Val	Gly	
109				325					330					335			
111	cga	ctc	att	gat	tac	att	cat	aaa	aac	gat	aat	gtt	caa	agg	gag	ctt	1056
112	Arg	Leu	Ile	Asp	Tyr	Ile	His	Lys	Asn	Asp	Asn	Val	Gln	Arg	Glu	Leu	
113			340					345					350				
115	cga	gac	tgg	ggg	ttg	agc	ttt	gat	tcc	aac	tta	ctg	tcc	ttc	tca	gga	1104
116	Arg	Asp	Trp	Gly	Leu	Ser	Phe	Asp	Ser	Asn	Leu	Leu	Ser	Phe	Ser	Gly	
117			355				360					365					
119	aga	att	ttg	caa	aca	gaa	aag	att	cac	caa	ggg	gga	aaa	aca	ttt	gat	1152
120	Arg	Ile	Leu	Gln	Thr	Glu	Lys	Ile	His	Gln	Gly	Gly	Lys	Thr	Phe	Asp	
121		370					375					380					
123	tac	aat	cca	caa	ttt	gca	gat	tgg	tcc	aaa	gaa	aca	aga	ggg	gca	cca	1200
124	Tyr	Asn	Pro	Gln	Phe	Ala	Asp	Trp	Ser	Lys	Glu	Thr	Arg	Gly	Ala	Pro	

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125 385          390          395          400
127 tta att agt gtt aag cca cta gat aac tgg ctg ttg atc tat acg cga      1248
128 Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg
129          405          410          415
131 aga aat tat gaa gca gcc aat tca ttg ata caa aat cta ttt aaa gtt      1296
132 Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val
133          420          425          430
135 aca cca gcc atg ggc atg caa atg aga aaa gca ata atg att gaa gtg      1344
136 Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val
137          435          440          445
139 gat gac aga act gaa gcc tac tta aga gtc tta cag caa aag gtc aca      1392
140 Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr
141          450          455          460
143 gca gac acc cag ata gtt gtc tgt ctg ttg tca agt aat cgg aag gac      1440
144 Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp
145 465          470          475          480
147 aaa tac gat gct att aaa aaa tac ctg tgt aca gat tgc cct acc cca      1488
148 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro
149          485          490          495
151 agt cag tgt gtg gtg gcc cga acc tta ggc aaa cag caa act gtc atg      1536
152 Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met
153          500          505          510
155 gcc att gct aca aag att gcc cta cag atg aac tgc aag atg gga gga      1584
156 Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly
157          515          520          525
159 gag ctc tgg agg gtg gac atc ccc ctg aag ctc gtg atg atc gtt ggc      1632
160 Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly
161          530          535          540
163 atc gat tgt tac cat gac atg aca gct ggg cgg agg tca atc gca gga      1680
164 Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly
165 545          550          555          560
167 ttt gtt gcc agc atc aat gaa ggg atg acc cgc tgg ttc tca cgc tgc      1728
168 Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys
169          565          570          575
171 ata ttt cag gat aga gga cag gag ctg gta gat ggg ctc aaa gtc tgc      1776
172 Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys
173          580          585          590
175 ctg caa gcg gct ctg agg gct tgg aat agc tgc aat gag tac atg ccc      1824
176 Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro
177          595          600          605
179 agc cgg atc atc gtg tac cgc gat ggc gta gga gac ggc cag ctg aaa      1872
180 Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys
181          610          615          620
183 aca ctg gtg aac tac gaa gtg cca cag ttt ttg gat tgt cta aaa tcc      1920
184 Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser
185 625          630          635          640
187 att ggt aga ggt tac aac cct aga cta acg gta att gtg gtg aag aaa      1968
188 Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys
189          645          650          655

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191 aga gtg aac acc aga ttt ttt gct cag tct gga gga aga ctt cag aat      2016
192 Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn
193          660          665          670
195 cca ctt cct gga aca gtt att gat gta gag gtt acc aga cca gaa tgg      2064
196 Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr Arg Pro Glu Trp
197          675          680          685
199 tat gac ttt ttt atc gtg agc cag gct gtg aga agt ggt agt gtt tct      2112
200 Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser
201          690          695          700
203 ccc aca cat tac aat gtc atc tat gac aac agc ggc ctg aag cca gac      2160
204 Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp
205 705          710          715          720
207 cac ata cag cgc ttg acc tac aag ctg tgc cac atc tat tac aac tgg      2208
208 His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp
209          725          730          735
211 cca ggt gtc att cgt gtt cct gct cct tgc cag tac gcc cac aag ctg      2256
212 Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu
213          740          745          750
215 gct ttt ctt gtt ggc cag agt att cac aga gag cca aat ctg tca ctg      2304
216 Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Leu
217          755          760          765
219 tca aac cgc ctt tac tac ctc taa      2328
220 Ser Asn Arg Leu Tyr Tyr Leu
221          770          775
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225 <211> LENGTH: 775
226 <212> TYPE: PRT
227 <213> ORGANISM: Homo sapiens
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232 1          5          10          15
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236          20          25          30
239 Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile
240          35          40          45
243 Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu
244          50          55          60
247 Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr
248 65          70          75          80
251 Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe
252          85          90          95
255 Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr
256          100          105          110
259 Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile
260          115          120          125
263 Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg
264          130          135          140
267 Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp Ile Pro Ser His Arg Leu
268 145          150          155          160

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271 Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser
272      165      170      175
275 Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr
276      180      185      190
279 Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys
280      195      200      205
283 Phe Gln Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr
284      210      215      220
287 Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln
288 225      230      235      240
291 Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe
292      245      250      255
295 Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys
296      260      265      270
299 Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg Gly Pro Gly Gly
300      275      280      285
303 Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr
304      290      295      300
307 Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu
308 305      310      315      320
311 Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly
312      325      330      335
315 Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu
316      340      345      350
319 Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly
320      355      360      365
323 Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp
324      370      375      380
327 Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro
328 385      390      395      400
331 Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg
332      405      410      415
335 Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val
336      420      425      430
339 Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val
340      435      440      445
343 Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr
344      450      455      460
347 Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp
348 465      470      475      480
351 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro
352      485      490      495
355 Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met
356      500      505      510
359 Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly
360      515      520      525
363 Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly
364      530      535      540
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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date